

Applicant: Yang Pan
Title: NOVEL MOLECULES OF THE TANGO-93-RELATED
PROTEIN FAMILY AND USES THEREOF
Attorney: Jean M. Silveri
Docket No.: MBIO98-048CP2CN1M
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GAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGGAGCCTGCTTTCTACTTAGGTCTCAAATTTTCCAGCCTTGTC 7

TTTGCCCTAAAATTTCTGCTGTTTATTTCAAATAGGGTCTACATACTGTGGAGCTC M M V L S
ATG ATG GTT CTG AGT 15

G A L C F R M K D S A L K V L Y L H N N 2
GGG GCA CTA TGC TTC CGA ATG AAG GAT TCA GCC TTG AAG GTA CTG TAT CTG CAC AAT AAC 21

Q L L A G G L H A E K V I K G E E I S V 4
CAG CTG CTG GCT GGA GGA CTG CAC GCA GAG AAG GTC ATT AAA GGT GAG GAG ATC AGT GTT 27

V P N R A L D A S L S P V I L G V Q G G 6
GTC CCA AAT CGG GCA CTG GAT GCC AGT CTG TCC CCT GTC ATC CTG GGC GTT CAA GGA GGA 33

S Q C L S C G T E K G P I L K L E P V N 8
AGC CAG TGC CTA TCT TGT GGG ACA GAG AAA GGG CCA ATT CTG AAA CTT GAG CCA GTG AAC 39

I M E L Y L G A K E S K S F T F Y R R D 10
ATC ATG GAG CTC TAC CTC GGG GCC AAG GAA TCA AAG AGC TTC ACC TTC TAC CGG CGG GAT 45

M G L T S S F E S A A Y P G W F L C T S 12
ATG GGT CTT ACC TCC AGC TTC GAA TCC GCT GCC TAC CCA GGC TGG TTC CTC TGC ACC TCA 51

P E A D Q P V R L T Q I P E D P A W D A 14
CCG GAA GCT GAC CAG CCT GTC AGG CTC ACT CAG ATC CCT GAG GAC CCC GCC TGG GAT GCT 57

P I T D F Y F Q Q C D * 15
CCC ATC ACA GAC TTC TAC TTT CAG CAG TGT GAC TAG 60

GGCTGCGTGGTCCCCAAAACCTCCATAAGCAGAGGCAGAGTAGGCAGTGGCGGCTCCTGATAGAGGATAGAGAGACAGAG 68

GAGCTCCACAGTAGGTGGCTTACTCCTCTCCTTCCCTACTGGACTCCCGCTTCTGACCTAAGGCACACAGACACTCTCT 76

TCTCCTGCATCCCAGTGCTGGTAAATCTTCTGGTATTTGGAGCTCAATGTGTAGATTCTTTTCTGATTGGATGGTACTAC 84

CTCTGGTGTGGAACCCAATAGAAACACGCTAGGACCAACAAAGAGCAACATAAAAGATTCTTGGGTGAAGAAGAGGTGG 92

GAACTGTTTCATACATAGTAAGATCTGACACAGTACCTCAGAAGTCCTGCCATTTCCTTATGTTCTGGAGAAAGTGGAGGG 100

GGGGTCACCAAGACTTTTCTCTGGCTGGCTGGGCCCTTTCCCTCAACCTTTCTGACATCTGCAGCCTCTCTCATTCTTGC 108

CTTCATTCTCTGGCCCTGAACCGAGAGGGTGATATCAGGATAGCTGACAGAAGATGACCAGGCACACTGTCCTGGTTTG 116

AAACCAGAGGGGACAATAAAAAACCTGATTCTGGTCTCTACTCACATAAAAAAGAAGCTTGTGAACATTAAGTGGGAAG 123

AGATTGCTACTAAATAACATACCTTGGAAATTCATCTTAATTAAAATATACTTCTCTATATTATATATTTTAAAAAAA 132

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACATGCGGCCG 136

FIG. 1

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| | | |
|---|---------------------|------|
| | M V L E G | 5 |
| ATCGACCCACGCGTCCGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAAG | ATG GTC CTG AGT GGG | 71 |
| | | |
| A L C F R M K D S A L K V L Y L H N N Q | | 25 |
| GCG CTG TGC TTC CGA ATG AAG GAC TCG GCA TTG AAG GTG CTT TAT CTG CAT AAT AAC CAG | | 131 |
| | | |
| L L A G G L H A G K V I K G E E I S V V | | 45 |
| CTT CTA GCT GGA GGG CTG CAT GCA GGG AAG GTC ATT AAA GGT GAA GAG ATC AGC GTG GTC | | 191 |
| | | |
| P N R W L D A S L S P V I L G V Q G G S | | 65 |
| CCC AAT CGG TGG CTG GAT GCC AGC CTG TCC CCC GTC ATC CTG GGT GTC CAG GGT GGA AGC | | 251 |
| | | |
| Q C L S C G V G Q E P T L T L E P V N I | | 85 |
| CAG TSC CTG TCA TGT GGG GTG GGG CAG GAG CCG ACT CTA ACA CTA GAG CCA GTG AAC ATC | | 311 |
| | | |
| N E L Y L G A K E E K S F T F Y R R D M | | 105 |
| ATG GAG CTC TAT CTT GGT GCC AAG GAA TCC AAG AGC TTC ACC TTC TAC CGG CGG GAC ATG | | 371 |
| | | |
| G L T S S F E S A A Y P G W F L C T V P | | 125 |
| GGG CTC ACC TCC AGC TTC GAG TCG GCT GCC TAC CCG GGC TGG TTC CTG TGC ACG GTG CCT | | 431 |
| | | |
| E A D Q P V R L T Q L P E N G G W N A P | | 145 |
| GAA GCC GAT CAG CCT GTC AGA CTC ACC CAG CTT CCC GAG AAT GGT GGC TGG AAT GCC CCC | | 491 |
| | | |
| I T D F Y F Q Q C D * | | 155 |
| ATC ACA GAC TTC TAC TTC CAG CAG TGT GAC TAG | | 524 |
| | | |
| GGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATC | | 603 |
| | | |
| ACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAGTGGGCACCTGACCACCTTTGTCTCTGGTTCCAGTTTGGATA | | 682 |
| | | |
| AATTTCTGAGATTTGGAGCTCAGTCCACGGTCCTCCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTA AAAACCATG | | 761 |
| | | |
| TGGGGTAAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGCTTAATG | | 840 |
| | | |
| GTAAGTGACAAGTGTTACCCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACA | | 919 |
| | | |
| TGAAGTCCTGTCACTCACTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCTTGGCCCAGCCCC | | 998 |
| | | |
| ACCCCTTCCCTTTAATCCTGCCACTGTCATATGCTACCTTTTCCTATCTCTCCCTCATCATCTTGTGTGGGCATGAG | | 1077 |
| | | |
| GAGGTGGTGATGTCAGAAGAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAAC | | 1156 |
| | | |
| TCAGATAACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAGACCTACTT | | 1235 |
| | | |
| ACAAAGTGGCATATATTGCAATTTATTTTAATTAAAGATACCTATTTATATATTTCTTTATAAAAAAAAAAAAAAAAAAAG | | 1314 |
| | | |
| GGCGGCCGC | | 1323 |

FIG. 2

```
ht93 1  MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWL 50
      |||
mt93 2  MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEESISVVPNRAL 51
      |||

ht93 51 DASLSPVILGVQGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTF 100
      |||
mt93 52 DASLSPVILGVQGSQCLSCGTEKGPIKLEPVNIMELYLGAKESKSFTF 101
      |||

ht93 101 YRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGAWNAPITDFY 150
      |||
mt93 102 YRRDMGLTSSFESAAYPGWFLCTSPEADQPVRLTQIPEDPAWDAPITDFY 151
      |||

ht93 151 FQQCD 155
      |||
mt93 152 FQQCD 156
```

FIG. 3

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------------|
| | 1 | | | | | 50 |
| mt93 | ----- | ----- | ----- | -----M | MVLSGALCFR | MKDSALKVLY |
| ht93 | ----- | ----- | ----- | ----- | MVLSGALCFR | MKDSALKVLY |
| illra-human | MEICRGLRSH | LITLLL.FLF | HSETICRPSG | RKSSKMQAFR | IWDVNQKTFY | |
| illra-mouse | MEICWGPYSH | LISLLLILLF | HSEAACRPSG | KRPCKMQAFR | IWDTNQKTFY | |
| | 51 | | | | | 100 |
| mt93 | LHNNQLLAGG | LHAEKVIKGE | EISVVPNRAL | DASLSPVILG | VQGSQCLSC | |
| ht93 | LHNNQLLAGG | LHAGKVIKGE | EISVVPNRWL | DASLSPVILG | VQGSQCLSC | |
| illra-human | LRNNQLVAGY | LQGPVNLEE | KIDVVP.... | .IEPHALFLG | IHGGKMCLSC | |
| illra-mouse | LRNNQLIAGY | LQGPNIKLEE | KIDMVP.... | .IDLHSVFLG | IHGGKLCLSC | |
| | 101 | | | | | 150 |
| mt93 | G.TEKGPIK | LEPVNIMELY | LGAKESKSFT | FYRRDMGLTS | SFESAAYPGW | |
| ht93 | G.VGQEPTLT | LEPVNIMELY | LGAKESKSFT | FYRRDMGLTS | SFESAAYPGW | |
| illra-human | VKSGDETRLQ | LEAVNITDLS | ENRKQDKRFA | FIRSDSGPTT | SFESAACPGW | |
| illra-mouse | AKSGDDIKLQ | LEEVNITDLS | KNKEEDKRFT | FIRSEKGPTT | SFESAACPGW | |
| | 151 | | | | | 186 |
| mt93 | FLCTSPEADQ | PVRLTQIPED | PAWDAPITDF | YFQQCD | | |
| ht93 | FLCTVPEADQ | PVRLTQLPEN | GGWNAPITDF | YFQQCD | | |
| illra-human | FLCTAMEADQ | PVSLTNMPDE | G...VMVTKF | YFQEDE | | |
| illra-mouse | FLCTTLEADR | PVSLTNTPEE | P...LIVTKF | YFQEDQ | | |

FIG. 4

| | | |
|---|---------|------|
| CCACAGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAAG | M V L S | 4 |
| G A L C F R M K D S A L K V L Y L H N N | | 24 |
| GGG GCG CTG TGC TTC CGA ATG AAG GAC TCG GCA TTG AAG GTG CTT TAT CTG CAT AAT AAC | | 134 |
| Q L L A G G L H A G K V I K G E E I S V | | 44 |
| CAG CTT CTA GCT GGA GGG CTG CAT GCA GGG AAG GTC ATT AAA GGT GAA GAG ATC AGC GTG | | 194 |
| V P N R W L D A S L S P V I L G V Q G G | | 64 |
| GTC CCC AAT CGG TGG CTG GAT GCC AGC CTG TCC CCC GTC ATC CTG GGT GTC CAG GGT GGA | | 254 |
| S Q C L S C G V G Q E P T L T L E P V N | | 84 |
| AGC CAG TGC CTG TCA TGT GGG GTG GGG CAG GAG CCG ACT CTA ACA CTA GAG CCA GTG AAC | | 314 |
| I M E L Y L G A K E S K S F T F Y R R D | | 104 |
| ATC ATG GAG CTC TAT CTT GGT GCC AAG GAA TCC AAG AGC TTC ACC TTC TAC CGG CGG GAC | | 374 |
| M G L T S S F E S A A Y P G W F L C T V | | 124 |
| ATG GGG CTC ACC TCC AGC TTC GAG TCG GCT GCC TAC CCG GGC TGG TTC CTG TGC ACG GTG | | 434 |
| P E A D Q P V R L T Q L P E N G G W N A | | 144 |
| CCT GAA GCC GAT CAG CCT GTC AGA CTC ACC CAG CTT CCC GAG AAT GGT GGC TGG AAT GCC | | 494 |
| P I T D F Y F Q Q C D * | | 156 |
| CCC ATC ACA GAC TTC TAC TTC CAG CAG TGT GAC TAG | | 530 |
| GGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATC | | 609 |
| ACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGATA | | 688 |
| AATTCTGAGATTTGGAGCTCAGTCCACGGTCCTCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTA AAAACCATG | | 767 |
| TGGGGTAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGCTTAATG | | 846 |
| GTAAGTGAAGTGTACCTGAGCCCGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACA | | 925 |
| TGAAGTCCTGTCACTCACCAGTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCTTGCCCCAGCCCC | | 1004 |
| ACCCCTTCCCTTTAATCCTGCCACTGTCTATGCTACCTTTCCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAG | | 1083 |
| GAGGTGGTGATGTGAGAAGAAATGGCTCGAGCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAAC | | 1162 |
| CCAAGATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTATGACATATTGAGAAGACCTACTT | | 1241 |
| ACAAAGTGGCATATATTGCAATTTATTTTAATTAAGATACCTATTTATATTTCTTTATAGAAAAAGTCTGGAAG | | 1320 |
| AGTTTACTTCAATTGTAGCAATGTGAGGTGGTGGCACTATAGGTGATTTTCTTTTAATTCTGTTAATTTATCTGTAT | | 1399 |
| TTCTAATTTTTCTACAATGAAGATGAATTCCTGTATAAAAAATAAGAAAAGAAATTAATCTTGACGTAAGCAGAGCAG | | 1478 |
| ACATCATCTCTGATTGTCTCAGCCTCACTTCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTGCTGGTTGGT | | 1557 |
| TGTAGTAGTGATCAGGAACAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCT | | 1636 |
| GGGTAAGGAACCTTAAGAACA AAAATCATCTGGTAATTTCTTCTAGAGGATCACAGCCCTGGGATTCCAAGGCATT | | 1715 |
| GGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCACATCCTTCTTGAATCTCAGTC | | 1794 |
| TGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAGTTAGTTAAGACAAGGTGATGCTGGATGAAGGTAGACCTAAA | | 1873 |
| TTCAATATGACTGGTTTCTTGTATGAAAGGAGAGGACACAGACAGAGGAGACCGGGGAAGACTATGTAAGATG | | 1952 |
| AAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCATCAGAAGCTTGAAGAGGC | | 2031 |
| AAAGAAGAATTCTTCCCAAGAATAAATTCGGCTGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAAC | | 2110 |
| TAATACAGCTGCTAAATGATCCCTGTCTCCTCGTGTTCATCTGTGTGTGTCCCCCTCCCAATGTACCAAGTTG | | 2189 |

FIG. 5A

TCTTTGTGACCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTCT 2268
ACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCCATG 2347
CTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCTGCCACAGCCACATTAGTGAACCTAGAAG 2426
CAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTTGGTCTAACTTGTT 2490

FIG. 5B

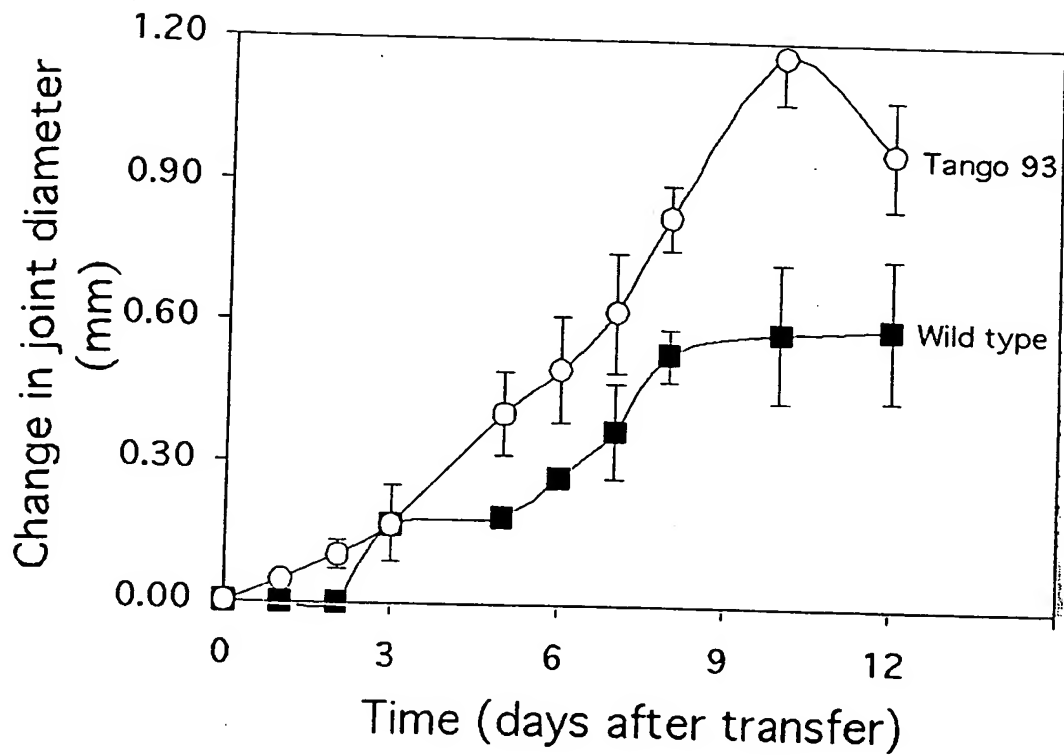


FIGURE 6